

Registration of Four Diverse Random-Mated Cotton Germplasm Populations

Lori L. Hinze,* Russell J. Kohel, B. Todd Campbell, and Richard G. Percy

ABSTRACT

Dwarf GP (Reg. No. GP-967; PI 669119), Fiber GP (Reg. No. GP-968; PI 669120), Glandless GP (Reg. No. GP-969; PI 669121), and Race GP (Reg. No. GP-970; PI 669122) are four unique upland cotton (*Gossypium hirsutum* L.) germplasm populations (GP) released by the USDA-ARS. Dwarf GP is a four-parent, narrow-based population developed to incorporate dwarfing genes into nondwarf genetic backgrounds. The remaining three populations are broad-based, complex populations. Fiber GP (24 parents) was developed to include potential sources of variation that would improve fiber length and strength. At the time these populations were developed, a viable glandless seed industry existed, and Glandless GP (22 parents) incorporated glandless germplasm from public and private breeders. Race GP (42 parents) was developed to obtain new genetic recombination events among a set of primitive race stock parents. These populations were created to recombine the variability from multiple parents into a single source from which selection can be initiated. Glandless GP was formed by random mating for nine cycles using a bulked pollen methodology. Dwarf GP, Fiber GP, and Race GP were formed by random mating for one cycle using a bulked pollen methodology followed by eight cycles using a male sterile. These populations possess trait specific and non-trait specific genetic diversity resulting from multiple generations of recombination and, therefore, present breeders with useful tools for improvement of elite germplasm.

FOUR UPLAND COTTON (*Gossypium hirsutum* L.) germplasm populations (GP), Dwarf GP (Reg. No. GP-967; PI 669119), Fiber GP (Reg. No. GP-968; PI 669120), Glandless GP (Reg. No. GP-969; PI 669121), and Race GP (Reg. No. GP-970; PI 669122), were developed by the USDA-ARS and released in March 2012. Each population was developed with the objective of making the variability found in multiple potential parents more accessible in the form of a single genetic resource, i.e., germplasm population. The properties of dwarfing, variable fiber quality, and glandless genotypes, along with the morphological diversity of the primitive cotton race stocks, were assessed by developing a pool of germplasm for each characteristic. Through random mating of multiple parents of divergent morphology, physiology, and adaptation, four genetically diverse germplasm populations were created. The majority of parents chosen were plant introductions (PIs) available from the U.S. National Cotton Germplasm Collection; in addition, parents were also chosen from breeding lines and cultivars developed by public institutions and private companies. One population, Dwarf GP, is a four-parent population; three—Fiber GP, Glandless GP, and Race GP—are complex populations formed by intermating 22 or more parents. All four populations were random mated for nine generations and segregated for important agronomic and fiber quality traits (Hinze et al., 2011). The populations are the result of decades of breeding efforts by numerous researchers and are designed to help breeders tap into the potential of the National Cotton Germplasm Collection. Because these populations contain a range of trait specific genetic variation in addition to a wide range of non-trait specific genetic diversity resulting from multiple generations of recombination, they present breeders with useful tools for broadening and improving elite germplasm pools.

Population formation is a “prebreeding” method of germplasm enhancement whereby useful genes and gene

Copyright © Crop Science Society of America. All rights reserved. No part of this periodical may be reproduced or transmitted in any form or by any means, electronic or mechanical, including photocopying, recording, or any information storage and retrieval system, without permission in writing from the publisher. Permission for printing and for reprinting the material contained herein has been obtained by the publisher.

Journal of Plant Registrations 8:57–62 (2014).
doi: 10.3198/jpr2013.06.0027crg

Received 6 June 2013. Registration by CSSA.
5585 Guilford Rd., Madison, WI 53711 USA

*Corresponding author (lori.hinze@ars.usda.gov)

L.L. Hinze, R.J. Kohel, and R.G. Percy, USDA-ARS, Southern Plains Agricultural Research Center, 2881 F&B Rd., College Station, TX 77845; B.T. Campbell, USDA-ARS, Coastal Plains Soil, Water, and Plant Research Center, 2611 West Lucas St., Florence, SC 29501. Mention of trade names or commercial products in this publication is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the U.S. Department of Agriculture.

Abbreviations: GP, germplasm population; HVI, High Volume Instrument; MAR, Multiple Adversity Resistance; SPARC, Southern Plains Agricultural Research Center.

combinations are pooled into usable phenotypes to make these resources more available. These semi-improved germplasm pools then become sources of variability for further cultivar development. The rationale for the creation of semi-improved pools of genetic diversity is to make the diversity present in inherently nonagronomic germplasm or underutilized crop genetic resources available for incorporation into elite breeding germplasm (Simmonds, 1993). This is a long-term strategy to create populations from non-elite germplasm by maximizing recombination, while allowing for adaptation to a given environment. When populations have been improved to a commercially viable level, they can be crossed to elite germplasm to introduce novel variation with minimal disruption of the elite background.

In addition to exploiting underutilized resources, these populations can be used to broaden the germplasm base of upland cotton. Recent reports have focused on the narrow germplasm base and relatedness among current cotton cultivars (Van Esbroeck et al., 1999; Bowman et al., 2006). Three of these populations have 22 or more parents, and all have undergone nine generations of intermating. The genetic diversity of the parents used to form a population and the generations of intermating before selection determine the potential genetic gain that can be realized with optimal selection within a population (Bernardo, 2002). Therefore, these populations theoretically have great potential to generate individuals with unique combinations of alleles.

Materials and Methods

Development of Populations

In forming Dwarf GP, the 'Lubbock Dwarf' line (Quisenberry, 1975) was used as the common parent and crossed to each of the three remaining parents in the population to introduce dwarfing genes into nondwarf backgrounds. The three individual crosses to Lubbock Dwarf were advanced to the F_3 generation without selection. The F_3 plants, 40 from each cross, were manually bulk crossed. For the bulk crossing, pollen was collected from all three F_3 families and bulked to pollinate each F_3 plant. Crossing was begun when all plants were flowering. The difference in the maturity of the lines required flower removal from the early plants until all were flowering.

Fiber GP, Glandless GP, and Race GP were formed by hybridizing all parents in a diallel system. The F_1 hybridizations occurred over several years beginning in the 1970s at the Southern Plains Agricultural Research Center (SPARC) in College Station, TX. Each F_1 cross involved was advanced to the F_3 generation without selection. In the F_3 generation, pollen was collected from each cross and bulked to pollinate each plant (as described above).

Bulked pollen methods have proven effective for developing random-mated cotton populations (Gutierrez et al., 2006). However, due to the complex and time-consuming nature of this bulked pollen method, a dominant male-sterile line (Male sterile 4, *Ms4*; Allison and Fisher, 1964) was introduced in the F_4 generation to facilitate crossing. *Ms4* was only used in Dwarf GP, Fiber GP, and Race GP. Glandless GP consisted of germplasm with recessive glandless genes—these recessive genes cannot be directly selected for together with the dominant

gene for male sterility. Therefore, the bulked pollen method of random mating was continued for eight additional cycles in the Glandless GP.

When used in the crossing blocks for Dwarf GP, Fiber GP, and Race GP, *Ms4* was planted in alternate rows with the respective GP. Plants from the germplasm pools contributed the pollen that fertilized the *Ms4* plants. Single bolls were harvested from individual sterile plants to obtain a minimum of 100 bolls. Seeds from these bolls were bulked, and a random sample was used to plant the next generation. No artificial selection was applied at any generation during population development. These three populations were advanced separately for eight additional cycles of random mating facilitated by the male-sterile. While using the male-sterile, populations consisted of ~200 plants with a minimum 21.5 m separation distance and pollinator rows to manage pollen flow from adjacent populations.

Evaluation of Diversity in Populations

Seed of the four germplasm populations was planted in three locations in 2009 using a randomized complete block design with three replications. The populations were grown at SPARC in College Station, TX; at the Texas A&M AgriLife Research Farm located near College Station, TX; and at the Clemson University Pee Dee Research and Education Center near Florence, SC. Soil type of the study area at SPARC was a Boonville fine sandy loam, 1 to 3% slopes. The Boonville soils are fine, smectitic, thermic Chromic Vertic Albaqualfs. Soil type at the Texas A&M Research Farm near College Station was a Ships silty clay, 0 to 1% slopes, a very-fine, mixed, active, thermic Chromic Hapluderts. Soil type at Clemson was Norfolk loamy sand (fine-loamy, kaolinitic, thermic Typic Kandiudults). At SPARC, field plots were 10.06 m by 1.02 m. For this location, seedlings were started in a greenhouse and then machine transplanted to the field with 20 plants per plot. At College Station, field rows were 12.19 m by 1.02 m, and at Florence, field rows were 10.67 m by 0.97 m. Experimental units at these two locations were two-row plots planted using direct seeding methods.

Diversity within each population was measured by collecting individual plant data from approximately 10% of the plants in each experimental unit, so each population was represented by approximately 78 plants across the three locations. Individual plant samples were used to calculate the agronomic properties of lint index (g), seed index (g), and boll size (g). High Volume Instrument (HVI) fiber properties were determined for individual plant samples by Starlab, Inc. (Knoxville, TN). These HVI fiber properties included upper half mean length (mm), micronaire (units), fiber strength (kN m kg⁻¹), and elongation (%). Total plots were harvested with mechanical pickers (except the SPARC location, which was harvested by hand), and these plot weights together with lint percent and plot area were used to determine lint yield (kg ha⁻¹). Germplasm population response was measured using a mixed model analysis of variance (PROC MIXED, SAS version 9.2; SAS Institute, Cary, NC), setting environments and populations as fixed effects and replications within environments as random effects.

Characteristics

The observed range of variation resulting from multiple diverse parents together with nine generations of intermating shows that these four germplasm populations are a valuable breeding resource. The means and ranges of trait values (Table 1) along with correlations (Hinze et al., 2011) shows the agronomic and fiber trait diversity within these four populations along with atypical relationships among some trait combinations. The correlation coefficients show that these populations express different relationships between traits than those commonly reported in the literature. For example, all four populations display nonsignificant relationships between lint yield and fiber length or strength. These results are at odds with results from studies of agronomically elite germplasm that often report negative relationships between yield components and fiber quality. Prior studies by Jenkins et al. (2008) also reported changes in correlations among traits after six cycles of random mating in a cotton population. The process of random mating, whether using bulked pollen (Jenkins et al., 2008) or male-sterile methodology, may change genetic relationships by reconfiguring epistatic interactions.

There was a general lack of significant differences among the four populations for agronomic and fiber traits, but high within population variation was observed for all populations. The development of diverse, multiple-parent populations was an efficient means of creating and identifying new and unique genotypes in genetic backgrounds that are useful for plant improvement. These and similar populations will allow breeders to more fully utilize resources available in the collection and in public breeding programs to improve cultivated cotton grown in the United States.

Dwarf GP

Dwarf GP is a four-parent population that was designed to introduce dwarfing genes into nondwarf backgrounds. A short-stature plant, Lubbock Dwarf, was crossed with Texas Marker-1 (Kohel et al., 1970; PI 607172), the *G. hirsutum* genetic standard; DORS, an okra leaf germplasm line with high yield potential and earliness, developed by the Texas A&M AgriLife Research Multiple Adversity Resistance (MAR) program; and Stoneville Okra Leaf, a noncommercial, extremely vegetative, and full-season okra leaf germplasm line developed by Stoneville Pedigreed Seeds. Dwarf GP had shorter observed plant heights (data not shown) and a narrow range of values for most traits when compared to the other three GPs (Table 1). Dwarf GP had the lowest lint index (mean = 4.85 g, $P < 0.05$; range = 3.74 g), smallest boll size (mean = 3.56 g, $P < 0.05$; range = 3.04 g), shortest fibers (mean = 24.53 mm, $P < 0.05$; range = 4.06 mm), and lowest micronaire (mean = 3.94 units, $P < 0.05$; range = 2.90 units).

Fiber GP

Fiber GP is a complex population developed from 24 parents with average to high fiber strength and short, medium, or long fiber length that flower during the summer at College Station, TX. The selected parents were PI 165244, PI 154088, PI 154096, PI 158562, PI 153966, PI 529808, PI 529809, PI 529810, PI 529811, PI 529814, PI 529815, PI 163654, PI 163742, PI 163693, PI 154050, and PI 154052 from the U.S. National Cotton Germplasm Collection in College Station, TX; PD 4461 (Q), PD 3364, Hybrid 330 (line F), and PD 9241 from the Pee Dee (PD) research program based in Florence, SC; and B1663-1, Acala 1028, B1627-1, and H2140-1 from the Acala research program based in Shafter, CA. Detailed source information for the parents can be found

Table 1. Population means and ranges for individual plants within populations of several important fiber and agronomic traits evaluated in three environments during 2009, including two locations near College Station, TX, and one location near Florence, SC.

Population	Mean†	Min.	Max.	Range	Population	Mean	Min.	Max.	Range
Upper half mean length (mm)					Lint yield (kg ha ⁻¹)				
Dwarf GP	24.53	22.61	26.67	4.06	Dwarf GP	474	178	871	693
Fiber GP	25.71	21.59	30.48	8.89	Fiber GP	502	232	834	602
Glandless GP	25.96	23.11	30.73	7.62	Glandless GP	484	136	863	727
Race GP	26.57	22.86	30.48	7.62	Race GP	581	201	1199	998
Micronaire (units)					Lint index (g)				
Dwarf GP	3.9	2.5	5.4	2.9	Dwarf GP	4.85	3.15	6.89	3.74
Fiber GP	4.4	2.6	5.9	3.3	Fiber GP	5.15	3.42	7.49	4.07
Glandless GP	4.7	2.7	6.1	3.4	Glandless GP	6.06	3.79	8.19	4.40
Race GP	4.3	2.8	6.0	3.2	Race GP	5.31	3.33	7.44	4.11
Strength (kN m kg ⁻¹)					Seed index (g)				
Dwarf GP	311.9	217.7	399.1	181.4	Dwarf GP	9.91	6.28	12.92	6.64
Fiber GP	310.5	223.6	380.5	156.9	Fiber GP	10.61	7.92	13.60	5.68
Glandless GP	327.8	234.4	459.9	225.6	Glandless GP	10.39	6.48	13.38	6.90
Race GP	313.1	226.5	410.9	184.4	Race GP	10.92	7.54	14.40	6.86
Elongation (%)					Boll Size (g)				
Dwarf GP	6.62	5.1	7.6	2.5	Dwarf GP	3.56	1.84	4.88	3.04
Fiber GP	6.76	5.3	8.2	2.9	Fiber GP	3.81	2.05	5.81	3.76
Glandless GP	6.67	5.3	7.8	2.5	Glandless GP	3.85	1.57	6.99	5.42
Race GP	6.68	5.4	7.9	2.5	Race GP	4.04	2.04	5.98	3.94

† Significant differences ($P < 0.05$) among population means were detected by analysis of variance for upper half mean length, micronaire, lint index, seed index, and boll size (Hinze et al., 2011). No significant differences among populations were measured for strength, elongation, or lint yield.

in Table 2. Parentage included 19 high strength lines and 5 average strength lines. Nine lines had long fibers, 5 lines had medium length fibers, and 10 lines had short fibers. This population had high variability in upper half mean length (mean = 25.71 mm; range = 8.89 mm) and elongation (mean = 6.76%; range = 2.9%) but the narrowest range of variability in fiber strength (mean = 310.5 kN m kg⁻¹; range = 156.9 kN m kg⁻¹), seed index (mean = 10.61 g; range = 5.68 g), and lint yield (mean = 502 kg ha⁻¹; range = 602 kg ha⁻¹). Our previous report suggested that the distribution of individual plant values for lint yield, boll size, lint index, and seed index in Fiber GP was non-normal, providing evidence that selection to change these traits could be effective (Hinze et al., 2011).

Glandless GP

Glandless GP is a complex population developed from 22 parents having the homozygous recessive *gl₂gl₃gl₃gl₃* genotype (Table 3). This genotype produces a phenotype with no gossypol glands in the hypocotyl and cotyledons of the seed (McMichael, 1960). The parents of this population came from one private and two public breeding programs. The selected parents were RDC, Rex glandless, LaAc × glandless, ‘Del Cerro’ (PI 529358) × Sampson × Stardelglandless × ‘Stoneville

213’ (PI 529229), (Del Cerro × Sampson × Stardel A)a, (Del Cerro × Sampson × Stardel A)b, Acala 7378-2/145 × 144 × D2 723-7, Del Cerro × Stardel A × Acala 7378, and (Del Cerro × Sampson × Stardel A) from Rogers Company in Waco, TX; Tx-GNORS-1-78, Tx-GNORS-2-78, Tx-ORSLY-2-78, and Tx-GNORH-1-78 from the MAR breeding program at Texas A&M University, College Station, TX; and G4684, G4941, G4953, G4975, G5244, G5257, G5281, (G4009 × G4570)F₂, and (G4078 × G4387)F₂ from the USDA breeding program in Shafter, CA. This population had the largest range of values for lint index (range = 4.4 g), seed index (range = 6.9 g), boll size (range = 5.42 g), micronaire (range = 3.4 units), and fiber strength (range = 225.5 kN m kg⁻¹). Individuals were observed in this GP with high fiber strength up to 459.9 kN m kg⁻¹. The Del Cerro parent would contribute to this as it is a high fiber strength germplasm (as good as pima cultivars available at the time) developed from New Mexico Acalas (Smith et al., 1999). Compared with the other populations, Glandless GP also had the highest lint index (mean = 6.06 g; *P* < 0.05) and micronaire (mean = 4.67 units; *P* < 0.05).

Table 2. Source information for 24 parents used to develop the Fiber GP. Parents with PI numbers are available from the U.S. National Cotton Germplasm Collection in College Station, TX, and background information (where available) for these parents, including race/variety name, plant exploration group, year, country, state, and site of collection, were obtained from the Germplasm Resources Information Network (GRIN) (USDA–ARS NGRP, 1993; J. Frelichowski, personal communication, 2012).

Designation	PI no.	Race/variety	Source	Year	Country	State	Site
High strength and long length							
Acala 1028			Acala lines, USDA–ARS (Shafter, CA)				
B1663-1			Acala lines, USDA–ARS (Shafter, CA)				
TX-0294	PI 165244	Latifolium	Manning and Ware Exploration	1948	Mexico	Oaxaca	Matatlan
Hybrid 330 (line F)			Pee Dee lines, USDA–ARS (Florence, SC)				
PD 3364			Pee Dee lines, USDA–ARS (Florence, SC)				
SA-1576	PI 529630	PD 4461Q	Pee Dee lines, USDA–ARS (Florence, SC)	1989	USA	South Carolina	Florence, PD Exp. Sta. USDA–ARS
High strength and medium length							
B1627-1			Acala lines, USDA–ARS (Shafter, CA)				
SA-1594	PI 606804	PD 9241 (Sub Okra)	Pee Dee lines, USDA–ARS (Florence, SC)	1986	USA	South Carolina	Florence, PD Exp. Sta. USDA–ARS
TX-0056	PI 154088	Latifolium	Richmond and Manning Exploration	1946	Mexico	Chiapas	Comitan de Dominguez
TX-0062	PI 154096	Latifolium	Richmond and Manning Exploration	1946	Mexico	Chiapas	San Bartolome
TX-0674	PI 158562		Stephens Collection	1947	Mexico	Yucatan	Merida
High strength and short length							
H2140-1			Acala lines, USDA–ARS (Shafter, CA)				
TX-0396	PI 529808	Hopi	King and Harrison Exploration	1989	USA	Arizona	Sacaton, from Moencopi in 1932
TX-0397	PI 529809	Hopi	King and Harrison Exploration	1989	USA	Arizona	Sacaton, from Moencopi in 1932
TX-0399	PI 529810	Hopi	King and Harrison Exploration	1989	USA	Arizona	Sacaton, from Moencopi in 1932
TX-0400	PI 529811	Hopi	King and Harrison Exploration	1989	USA	Arizona	Sacaton, from Moencopi in 1932
TX-0406	PI 529814	Hopi	King and Harrison Exploration	1989	USA	Arizona	Sacaton, from Moencopi in 1932
TX-0408	PI 529815	Hopi	King and Harrison Exploration	1989	USA	Arizona	Sacaton, from Moencopi in 1932
TX-0072	PI 153966	Latifolium	Richmond and Manning Exploration	1946	Guatemala	Suchitepequez	San Jose el Idolo
Average strength and long length							
TX-0093	PI 163654	Latifolium	Manning and Ware Exploration	1948	Guatemala	Jutiapa	Santa Catarina Mita
TX-0180	PI 163742	Latifolium	Manning and Ware Exploration	1948	Guatemala	Santa Rosa	
TX-0239	PI 163693	Latifolium	Manning and Ware Exploration	1948	Guatemala	Chiquimula	Chiquimula
Average strength and short length							
TX-0036	PI 154050	Latifolium	Richmond and Manning Exploration	1946	Mexico	Chiapas	Acala
TX-0039	PI 154052	Latifolium	Richmond and Manning Exploration	1946	Mexico	Chiapas	Acala

Table 3. Source information for 22 parents used to develop the Glandless GP.

Designation	Source
RDC	L Barton, Rogers Co. (Waco, TX)
Rex glandless	L Barton, Rogers Co. (Waco, TX)
LaAc × glandless	L Barton, Rogers Co. (Waco, TX)
Del Cerro × Sampson × Stardel glandless × Stoneville 213	L Barton, Rogers Co. (Waco, TX)
(Del Cerro × Sampson × Stardel A)a	L Barton, Rogers Co. (Waco, TX)
(Del Cerro × Sampson × Stardel A)b	L Barton, Rogers Co. (Waco, TX)
Acala 7378-2/145 × 144 × D2 723-7	L Barton, Rogers Co. (Waco, TX)
Del Cerro × Stardel A × Acala 7378	L Barton, Rogers Co. (Waco, TX)
(Del Cerro × Sampson × Stardel A)	L Barton, Rogers Co. (Waco, TX)
Tx-GNORS-1-78	LS Bird, TAMU (College Station, TX)
Tx-GNORS-2-78	LS Bird, TAMU (College Station, TX)
Tx-ORSLY-2-78	LS Bird, TAMU (College Station, TX)
Tx-GNORH-1-78	LS Bird, TAMU (College Station, TX)
G4684	A Hyer, USDA-ARS (Shafter, CA)
G4941	A Hyer, USDA-ARS (Shafter, CA)
G4953	A Hyer, USDA-ARS (Shafter, CA)
G4975	A Hyer, USDA-ARS (Shafter, CA)
G5244	A Hyer, USDA-ARS (Shafter, CA)
G5257	A Hyer, USDA-ARS (Shafter, CA)
G5281	A Hyer, USDA-ARS (Shafter, CA)
(G4009 × G4570)F ₂	A Hyer, USDA-ARS (Shafter, CA)
(G4078 × G4387)F ₂	A Hyer, USDA-ARS (Shafter, CA)

Race GP

Race GP is a complex population developed from 42 parents with high fiber strength and long fiber length among the cotton race stocks that are nonphotoperiodic at College Station, TX. The cotton race stocks are a group of primitive accessions collected from the Mesoamerican center of morphological diversity of upland cotton (Brubaker et al., 1999). These accessions are the original gene pool from which selections were made to develop modern cotton cultivars. The race stocks used in Race GP and source information for the parents can be found in Table 4. This population had significantly long fibers (26.57 mm, $P < 0.05$) and the largest range of lint yield values (mean = 581 kg ha⁻¹; range = 998 kg ha⁻¹). For lint yield, values in the upper tail of the distribution included transgressive segregates that would suggest selection would be effective to improve lint yield in this population (Hinze et al., 2011).

Availability

Small quantities of seed (25–50 g) are available to cotton breeders, geneticists, and other research personnel on written request to Lori Hinze, USDA-ARS, Southern Plains Agricultural Research Center, 2881 F&B Road, College Station, TX 77845. We suggest that interested persons should plant all seed received for these heterogeneous populations and bulk harvest one boll or locule from each plant to form a larger population from which to make subsequent selections and to maintain these populations for continued use. It is requested that appropriate recognition of the source be given when these germplasm populations contribute to the development of a new breeding line, hybrid, or cultivar. Genetic material of these released populations

will be deposited in the National Plant Germplasm System, where it will be available for research purposes.

Acknowledgments

This research project was supported by funding from CRIS No. 6202-21000-031-00D of the U.S. Department of Agriculture. The authors gratefully acknowledge support staff from the USDA-ARS cotton genetics and breeding projects in College Station, TX, and Florence, SC, for their valuable technical assistance during development of and/or evaluation of these populations.

References

- Allison, D.C., and W.D. Fisher. 1964. A dominant gene for male-sterility in upland cotton. *Crop Sci.* 4:548–549. doi:10.2135/cropsci1964.0011183X000400050035x
- Bernardo, R. 2002. *Breeding for quantitative traits in plants*. Stemma Press, Woodbury, MN.
- Bowman, D.T., O.A. Gutierrez, R.G. Percy, D.S. Calhoun, and O.L. May. 2006. Pedigrees of upland and pima cotton cultivars released between 1970 and 2005. *Bull.* 1155. Mississippi Agric. & For. Exp. Stn., Mississippi State.
- Brubaker, C.L., F.M. Bourland, and J.F. Wendel. 1999. The origin and domestication of cotton. In: C.W. Smith and J.T. Cothren, editors, *Cotton: Origin, history, technology, and production*. John Wiley & Sons, New York. p. 1–31.
- Gutierrez, O.A., D.T. Bowman, C.B. Cole, J.N. Jenkins, J.C. McCarty, J. Wu, and C.E. Watson. 2006. Development of random mated populations using bulked pollen methodology: Cotton as a model. *J. Cotton Sci.* 10:175–179.
- Hinze, L.L., R.J. Kohel, B.T. Campbell, and R.G. Percy. 2011. Variability in four diverse cotton (*Gossypium hirsutum* L.) germplasm populations. *Genet. Resour. Crop Evol.* 58:561–570. doi:10.1007/s10722-010-9599-8
- Jenkins, J.N., J.C. McCarty, Jr., O.A. Gutierrez, R.W. Hayes, D.T. Bowman, C.E. Watson, and D.C. Jones. 2008. Registration of RMUP-C5, a random mated population of upland cotton germplasm. *J. Plant Reg.* 2:239–242. doi:10.3198/jpr2008.02.0080crg
- Kohel, R.J., T.R. Richmond, and C.F. Lewis. 1970. Texas Marker-1: Description of a genetic standard for *Gossypium hirsutum* L. *Crop Sci.* 10:670–671. doi:10.2135/cropsci1970.0011183X001000060019x

Table 4. Source information for 42 parents used to develop the Race GP. Parents with PI numbers are available from the U.S. National Cotton Germplasm Collection, and background information (where available), including race, plant exploration group, year, country, state, and site of collection, were obtained from the Germplasm Resources Information Network (GRIN; USDA–ARS NGRP, 1993; J. Frelichowski, personal communication, 2012).

Designation	PI no.	Race	Source	Year	Country	State	Site
TX-0017	PI 154022	Latifolium	Richmond and Manning Exploration	1946	Mexico	Chiapas	Huitipan
TX-0021	PI 549148	Latifolium	Richmond and Manning Exploration	1946	Mexico	Chiapas	Inxtla
TX-0024	PI 154033	Latifolium	Richmond and Manning Exploration	1946	Mexico	Chiapas	Inxtla
TX-0031	PI 154045	Latifolium	Richmond and Manning Exploration	1946	Mexico	Chiapas	Acala
TX-0034	PI 154048	Latifolium	Richmond and Manning Exploration	1946	Mexico	Chiapas	Acala
TX-0035	PI 154049	Latifolium	Richmond and Manning Exploration	1946	Mexico	Chiapas	Acala
TX-0036	PI 154050	Latifolium	Richmond and Manning Exploration	1946	Mexico	Chiapas	Acala
TX-0038	PI 549149	Latifolium	Richmond and Manning Exploration	1946	Mexico	Chiapas	Acala
TX-0039	PI 154052	Latifolium	Richmond and Manning Exploration	1946	Mexico	Chiapas	Acala
TX-0040	PI 549150	Latifolium	Richmond and Manning Exploration	1946	Mexico	Chiapas	Acala
TX-0043	PI 154054	Latifolium	Richmond and Manning Exploration	1946	Mexico	Chiapas	Acala
TX-0056	PI 154088	Latifolium	Richmond and Manning Exploration	1946	Mexico	Chiapas	Comitan de Dominguez
TX-0057	PI 154090	Latifolium	Richmond and Manning Exploration	1946	Mexico	Chiapas	San Bartalome
TX-0062	PI 154096	Latifolium	Richmond and Manning Exploration	1946	Mexico	Chiapas	San Bartalome
TX-0063	PI 154099	Latifolium	Richmond and Manning Exploration	1946	Mexico	Chiapas	Flores Magon
TX-0064	PI 154100	Latifolium	Richmond and Manning Exploration	1946	Mexico	Chiapas	Rosario
TX-0065	PI 154101	Latifolium	Richmond and Manning Exploration	1946	Mexico	Chiapas	Rosario
TX-0067	PI 154103	Latifolium	Richmond and Manning Exploration	1946	Mexico	Chiapas	Lazara, Cardenas
TX-0072	PI 153966	Latifolium	Richmond and Manning Exploration	1946	Guatemala	Suchitepequez	San Jose el Idolo
TX-0093	PI 163654	Latifolium	Manning and Ware Exploration	1948	Guatemala	Jutiapa	Santa Catarina Mita
TX-0116	PI 163602			1948	Guatemala		
TX-0180	PI 163742	Latifolium	Manning and Ware Exploration	1948	Guatemala	Santa Rosa	
TX-0203	PI 165322	Latifolium	Manning and Ware Exploration	1948	Mexico	Oaxaca	Tototapan
TX-0206	PI 165368	Latifolium	Manning and Ware Exploration	1948	Mexico	Guerrero	Maquina del Rio de Niepa
TX-0226	PI 165369	Latifolium	Manning and Ware Exploration	1948	Mexico	Guerrero	Maquina del Rio de Niepa
TX-0239	PI 163693	Latifolium	Manning and Ware Exploration	1948	Guatemala	Chiquimula	Chiquimula
TX-0244	PI 165341	Latifolium	Manning and Ware Exploration	1948	Mexico	Oaxaca	Ixcopa
TX-0294	PI 165244	Latifolium	Manning and Ware Exploration	1948	Mexico	Oaxaca	Matatlan
TX-0375	PI 162895	Latifolium	Hartley and Stephens Exploration	1948	Paraguay		25 miles SE of Asuncion
TX-0396	PI 529808	Hopi	King and Harrison Exploration	1989	USA	Arizona	Sacaton-from Moencopi in 1932
TX-0397	PI 529809	Hopi	King and Harrison Exploration	1989	USA	Arizona	Sacaton-from Moencopi in 1932
TX-0399	PI 529810	Hopi	King and Harrison Exploration	1989	USA	Arizona	Sacaton-from Moencopi in 1932
TX-0400	PI 529811	Hopi	King and Harrison Exploration	1989	USA	Arizona	Sacaton-from Moencopi in 1932
TX-0401	PI 529812	Hopi	King and Harrison Exploration	1989	USA	Arizona	Sacaton-from Moencopi in 1932
TX-0404	PI 529813	Hopi	King and Harrison Exploration	1989	USA	Arizona	Sacaton-from Moencopi in 1932
TX-0406	PI 529814	Hopi	King and Harrison Exploration	1989	USA	Arizona	Sacaton-from Moencopi in 1932
TX-0408	PI 529815	Hopi	King and Harrison Exploration	1989	USA	Arizona	Sacaton-from Moencopi in 1932
TX-0409	PI 529816	Hopi	Mr. Killough	1989	USA	Arizona	Sacaton
TX-0622	PI 154078		Richmond Exploration	1946	Mexico		
TX-0624	PI 154104		Richmond Exploration	1946	Mexico	Chiapas	Lazara, Cardenas
TX-0674	PI 158562		Stephens Collection	1947	Mexico	Yucatan	Merida
TX-0709	PI 265146		Stephens Collection	1960	Nicaragua	Chinandega	Chinandega

McMichael, S.C. 1960. Combined effects of the glandless genes *gl₂* and *gl₁* on pigment glands in the cotton plant. *Agron. J.* 52:385–386. doi:10.2134/agronj1960.00021962005200070005x

Quisenberry, J.E. 1975. Inheritance of plant height in cotton: I. A cross between Lubbock Dwarf and Texas Marker-1. *Crop Sci.* 15:197–199. doi:10.2135/cropsci1975.0011183X001500020016x

Simmonds, N.W. 1993. Introgression and incorporation: Strategies for the use of crop genetic resources. *Biol. Rev. Camb. Philos. Soc.* 68:539–562. doi:10.1111/j.1469-185X.1993.tb01243.x

Smith, C.W., R.G. Cantrell, H.S. Moser, and S.R. Oakley. 1999. History of cultivar development in the United States. In: C.W. Smith and J.T. Cothren, editors, *Cotton: Origin, history, technology, and production*. John Wiley & Sons, New York. p. 150–151.

USDA–ARS NGRP. 1993. Germplasm Resources Information Network (GRIN) database. National Germplasm Resources Laboratory, Beltsville, MD. <http://www.ars-grin.gov> (accessed 5 Mar 2011).

Van Esbroeck, G.A., D.T. Bowman, O.L. May, and D.A. Calhoun. 1999. Genetic similarity indices for ancestral cotton cultivars and their impact on genetic diversity estimates of modern cultivars. *Crop Sci.* 39:323–328.